



SEQUENCE LISTING

<110> Bruce, Wesley B.

<120> A Nitrate-Responsive Root Transcriptional Factor

<130> 1263

<140> US 09/970,624

<141> 2001-10-04

<150> US 60/238,292

<151> 2000-10-05

<160> 3

www. Fast SEO for Windows Version 4.0

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210 1
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<213> DNA

<212> DNN

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<221> CDS

<222> (360) ... (1082)

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120
180
240
300
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407

cgg cag gtg acc ttc tcc aag cg^c cg^g aac gg^g atc tt^c aag aag gg^c
Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Ile Phe Lys Lys Ala
20 25 30

503

aag gag ctc gcc atc ctc tgc gat gcg gag gtc ggc ctc gtc atc ttc
Lys Glu Leu Ala Ile Leu Cys Asp Ala Glu Val Gly Leu Val Ile Phe
 35 40 45

551

55
tcc agc acc ggc cgc ctc tac gag tac tct agc acc agc atg aaa tca
Ser Ser Thr Gly Arg Leu Tyr Glu Tyr Ser Ser Thr Ser Met Lys Ser
55 60

599

gtt ata gat cgg tac ggc aag gcc aag gaa gag cag caa gtc gtc gca
 Val Ile Asp Arg Tyr Gly Lys Ala Lys Glu Glu Gln Gln Val Val Ala
 65 70 75 80

85	90	95		
aga caa caa ctg cac aac ttg caa gaa aat tat	cggtt acggaa			
Arg Gln Gln Leu His Asn Leu Gln Glu Asn Tyr Arg Gln	Gly Leu Thr Gly		695	
100	105	110		
gat gat ctt tct tgg ctg aat gtc aac gaa ctg cag tcc	ctgtt gag aat		743	
Asp Asp Leu Ser Gly Leu Asn Val Lys Glu Leu Gln Ser	Leu Glu Asn			
115	120	125		
caa ttg gaa aca aca agt ctg cgt ggt gtc cgc gca aag	aag gac cat ctc		791	
Gln Leu Glu Thr Ser Leu Arg Gly Val Arg Ala Lys Lys	Asp His Leu			
130	135	140		
ttg ata gat gag att cac gat ttg aat cga aag gca agt	tta tt cac		839	
Leu Ile Asp Glu Ile His Asp Leu Asn Arg Lys Ala Ser	Leu Phe His			
145	150	155	160	
caa gaa aat aca gac ttg tac aat aag atc aac ctg att	cgc caa gaa		887	
Gln Glu Asn Thr Asp Leu Tyr Asn Lys Ile Asn Leu Ile	Arg Gln Glu			
165	170	175		
aat gat gag tta cat aaa aag ata tat gag act gaa gga	cca agt gga		935	
Asn Asp Glu Leu His Lys Lys Ile Tyr Glu Thr Glu Gly	Pro Ser Gly			
180	185	190		
qtt aat cggtt gag tca ccg act cca ttc aac ttt gca gta	gta gaa acc		983	
Val Asn Arg Glu Ser Pro Thr Pro Phe Asn Phe Ala Val	Val Glu Thr			
195	200	205		
aga gat gtt cct gtg caa ctt gaa ctc agc aca ctg cca	cag caa aat		1031	
Arg Asp Val Pro Val Gln Leu Glu Leu Ser Thr Leu Pro	Gln Gln Asn			
210	215	220		
aac att gag cca tct act gct cct aag cta gga ttg caa	tta att cca		1079	
Asn Ile Glu Pro Ser Thr Ala Pro Lys Leu Gly Leu Gln	Ile Pro			
225	230	235	240	
tga agaagagtaa aactgccgtc ttatgtatgtt gaaggaaact	atttatttgtt		1132	
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aagatgtatgtt actcacagaaaa agacatattt	gtggcagggat gatttgatgtt atgaacttat		1192	
aaatgtatgtt caataatattt tcagacccga atggggtcgt	gaaatttcaga ggatgttgc		1252	
tttctaaaaaaa aaaaaaaaaaaaaaaa			1280	
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Met Gly Arg Gly Lys Ile Val Ile Arg Arg Ile Asp Asn Ser	Thr Ser			
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Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Ile Phe	Lys Lys Ala			
20	25	30		
Lys Glu Leu Ala Ile Leu Cys Asp Ala Glu Val Gly Leu	Val Ile Phe			
35	40	45		

Ser Ser Thr Gly Arg Leu Tyr Glu Tyr Ser Ser Thr Ser Met Lys Ser
50 55 60
Val Ile Asp Arg Tyr Gly Lys Ala Lys Glu Glu Gln Gln Val Val Ala
65 70 75 80
Asn Pro Asn Ser Glu Leu Lys Phe Trp Gln Arg Glu Ala Ala Ser Leu
85 90 95
Arg Gln Gln Leu His Asn Leu Gln Glu Asn Tyr Arg Gln Leu Thr Gly
100 105 110
Asp Asp Leu Ser Gly Leu Asn Val Lys Glu Leu Gln Ser Leu Glu Asn
115 120 125
Gln Leu Glu Thr Ser Leu Arg Gly Val Arg Ala Lys Lys Asp His Leu
130 135 140
Leu Ile Asp Glu Ile His Asp Leu Asn Arg Lys Ala Ser Leu Phe His
145 150 155 160
Gln Glu Asn Thr Asp Leu Tyr Asn Lys Ile Asn Leu Ile Arg Gln Glu
165 170 175
Asn Asp Glu Leu His Lys Lys Ile Tyr Glu Thr Glu Gly Pro Ser Gly
180 185 190
Val Asn Arg Glu Ser Pro Thr Pro Phe Asn Phe Ala Val Val Glu Thr
195 200 205
Arg Asp Val Pro Val Gln Leu Glu Leu Ser Thr Leu Pro Gln Gln Asn
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Asn Ile Glu Pro Ser Thr Ala Pro Lys Leu Gly Leu Gln Leu Ile Pro
225 230 235 240

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<213> Artificial Sequence

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36